

Supplementary figures

Nrm1	1	34	RDYSELSKKLQIRLQFAYYKYKTKQTDKNFTDLK
sbay_21681	1	34	KDYSELSKKLQIRLQFAYYKYKTKQTNKKFTDLK
Q6FQJ4_CANGA	1	34	AHYTELSKKLQIRLQLAYYKYRTKQEHVKFNELK
Q6CL21_KLULA	1	34	KLTDENILRLRSRVQLAYYKYRTKQVHLKFSEIV
Kwal_6092	1	34	VNFDQVADKLRI RMQLAYYK LKTKQGH LQFRQLK
Q6CHG8_YARLI	1	34	GKIREHADRLKMRLQLALYKINTKQTNVSLAALE
<i>S. pombe</i> Nrm1	1	34	DDIQCCAKNLRRLRELAM YKVQVNQTF SPLQDLP
Q4I804_GIBZE	1	34	PPAATRAETLRLRLSLANYKVRTGQTTVPLSELQ
Q52BB9_MAGGR	1	34	ELTRQTAETLRLRLRLAAYK LKTGQADVPLEQLQ
Q7RYK4_NEUCR	1	34	QAARQKAEILRLRLSLAAYKIQTGQTDVPLEQLE
Q5B3H8_EMENI	1	34	QFIQEKATLLRSRLQNAMRRVRDPQFDRRLSELE
Sr13	1	34	DSVREFSRTLKSRLNCAMV KLSKEHEQVALIPPP
Q6CNE8_KLULA	1	34	KPIREISNNLKSRLNYAYVKMQQNMLQHSKRGLD
Whi5	1	34	RPIREISHTLRTRLNYALVKLQNGWTDKTLPELE
Q6FMS3_CANGA	1	34	KPIKEISNELKTRLNYALMKLQNGWVDKSLPELE
Q759P2_ASHGO	1	34	KPIREISFNLKTRLNYAFVKLQNGWQDKTLPELE
Kwal_19749	1	34	KPIREISNNLKTRLSYAFVKLQNGWVDKTLPELE
Q4P866_USTMA	1	34	HEVEMYAHALRTRLQFASF KALNGV GKTSLSDLT
Q4I8U0_GIBZE	1	34	AEVSKIARRLQNRLALAKFKTKHGWEDLTLD SIE
Q75472_NEUCR	1	34	VEISRMVRRLQNRLALAQFKTKHGLEDLTLD SIE
Q874Y1_PODAN	1	34	AEISKMARRLQNRLALAQFKTKHGLEDLTLDKIE
Q6CGX3_YARLI	1	34	AEISRMTRNLKSRLKLATYKTKRGWDNLTFDTIE
Q55IU7_CRYNE	1	34	VELEKKMHQLQQRLELASVKASNGWTDLSVKEIE
Q4IJZ5_GIBZE	1	34	GHIGELSNE LRTRLSYAMVKVNNGWQSNSLEEVE
Q51ST0_MAGGR	1	34	SRMGELSHELKARLSYAMVKVNNGWESH S IDEVE
Q7S3U0_NEUCR	1	34	SRLGELSAELKTRLSYAMVKVNNGWQSHSIDQVE
Q4P797_USTMA	1	34	TRLLALS KHLMTRLQYANFKVEHGW SKQSLSEVE
Q9HGL9_SCHPO	1	34	TFEYKLSNKLRLARLKAFFKVDHGWEDQTL DQVE
Q6CFA6_YARLI	1	34	SDNEKLAAMRTRLNFAMVKVQKGWEDRSIDQIE
<i>C. albicans</i>	1	28	DTIGLAATK LKLKLQLALYKVQQNKQTR.....
<i>D. hansenii</i>	1	28	ATAGLAATK LKLKLQLAFYKLQHKSNSI.....

Fig. S1. Identification of Whi5 / Nrm1 homologs. In order to identify potential Whi5 homologs in the *C. albicans* genome, we used the generalized profile method (Bucher *et al.*, 1996), starting from a multiple alignment of *S. cerevisiae* Whi5 and its obvious homologs from other yeast species, including *S. pombe* Nrm1. After five cycles of iterative profile refinement, a conserved sub-region of the Whi5 family was identified to be present in several fungal proteins without overt sequence similarity to Whi5. The full sequences of the proteins aligned in this figure, together with additional *Candida spp.* homologous sequences, can be found in Table S4.

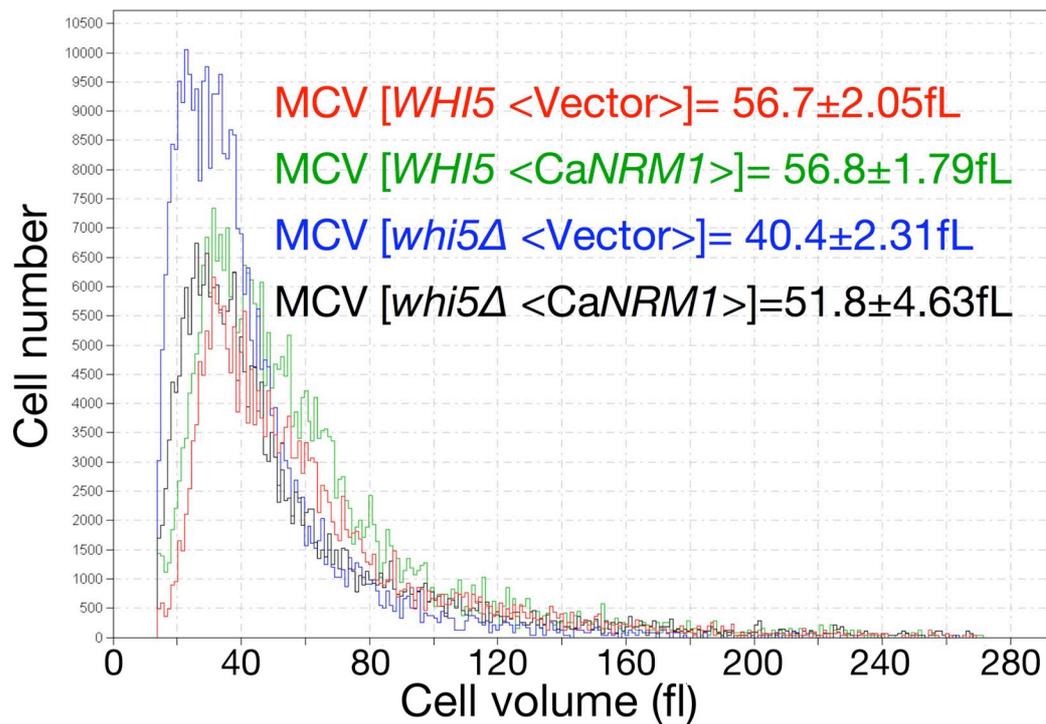


Fig. S2. CaNrm1 can complement the reduced cell size phenotype of *S. cerevisiae whi5Δ*.

The *S. cerevisiae whi5Δ* strain (Y01859) and its isogenic wild-type (BY4741) were transformed with either the *CaNRM1*-carrying plasmid KB1879 or the B2201 vector plasmid. Cells were grown to log phase, and tested as described in *Methods*. Representative curves of a single experiment are shown; the Mean Cell Volume (MCV) data represent the average +/- SD of 6 experiments.

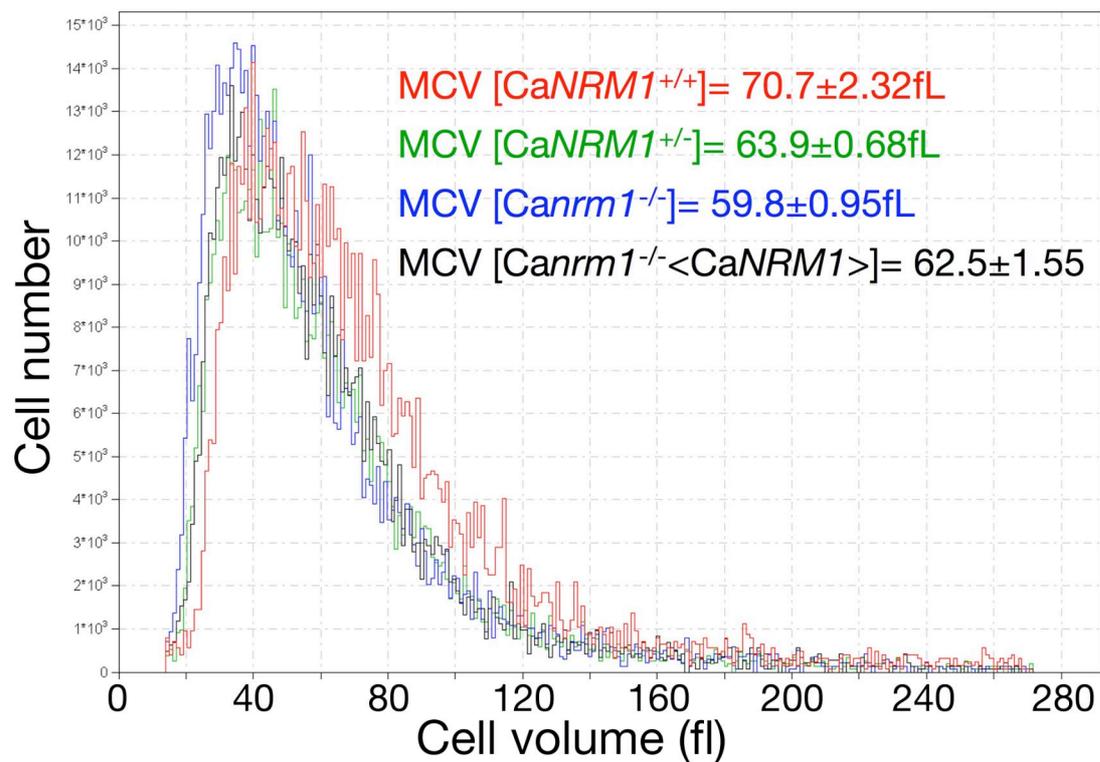


Fig. S3. CaNrm1 affects cell size in *C. albicans*. Cell size analysis of the *Canrm1*^{-/-} mutant (KC356) vs. heterozygote (KY352), wild-type (CAI4 <CaURA3>) and reintegant (KC436). Cells were grown to log phase, and tested as described in *Methods*. Representative curves of a single experiment are shown; the Mean Cell Volume (MCV) data represent the average +/- SD of 6 experiments.

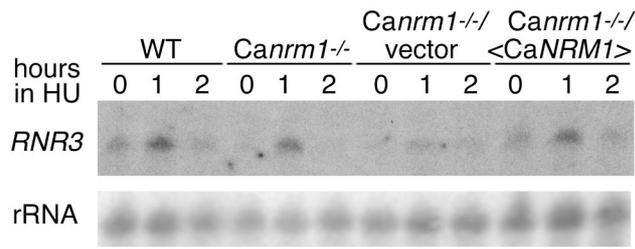


Fig. S4. Effect of CaNRM1 deletion and HU (200 mM) on *RNR3* expression

(orf19.5845). Cells were exposed to 200 mM HU for the indicated amounts of time.

Northern blotting was performed to assess the induction of *RNR3*. rRNA hybridization

served as loading control. The low signal level precluded quantitation by phosphorimager.

The strains are indicated as follows: + = CAI4 (wild-type); Δ = KC392 (*Canrm1*^{-/-}); Δ/v is

KC392 transformed with vector plasmid pBES116; and Δ/+ is KC392 transformed with the

CaNRM1 plasmid KB1993.

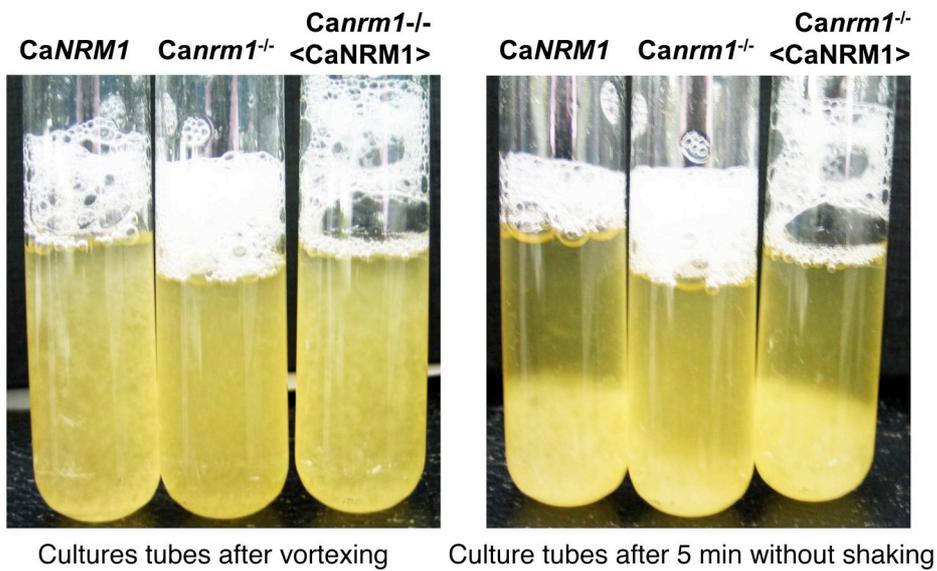


Fig. S5. Sedimentation. The indicated strains were grown overnight in YPD, then diluted 1:10 in YPD + 10% serum and grown for 2 h at 30°C. The test tubes were photographed right after retrieval from the roller drum and vigorous vortexing, or after having been left standing 5 min on the bench. The strains used are KC403, KC435, KC436 (all Ura+).

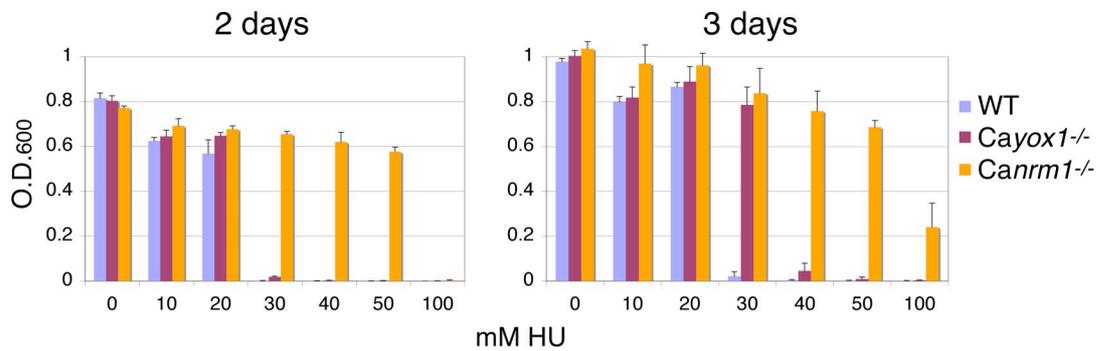


Fig. S6. Effect of CaYOX1 deletion on HU resistance. The CaYOX1 deletion mutant and its isogenic wild-type strain, as well as the CaNRMI deletion strains for comparison, were grown in quadruplicate at the indicated concentrations of HU at 30°C. O. D. was measured after 2 and 3 days, as indicated.